



37993.txt
SEQUENCE LISTING

<110> Loughney, Kate

<120> Phosphodiesterase 10

<130> 27866/35308

<140> 09/256,000

<141> 1999-02-23

<150> 60/075,508

<151> 1998-02-23

<160> 26

<170> PatentIn Ver. 2.0

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<211> 1548

<212> DNA

<213> Homo sapiens

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<222> (26)..(1423)

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aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta 100

Lys val Arg Pro val Ala ile Lys Gln Leu Ser Glu Arg Glu Glu Leu

10

15

25

atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc 148
Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
30 35 40

aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta 196
Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
45 50 55

gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa 244
Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
60 65 70

tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc 292
Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
75 80 85

agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag 340
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
90 95 100 105

aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc 388
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
110 115 120

tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg 436
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
125 130 135

ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac 484
Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His
140 145 150

gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg 532
 Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg
 155 160 165

agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac 580
 Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His
 170 175 180 185

aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc 628
 Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val
 190 195 200

tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc 676
 Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile
 205 210 215

cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac 724
 Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn
 220 225 230

aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat 772
 Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn
 235 240 245

gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc 820
 Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile
 250 255 260 265

ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg 868
 Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly
 270 275 280

ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac 916
 Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp

atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag 964
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu
300 305 310

aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att 1012
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile
315 320 325

ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc 1060
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val
330 335 340 345

gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc 1108
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser
350 355 360

gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga 1156
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg
365 370 375

gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc 1204
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
380 385 390

ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag 1252
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
395 400 405

gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag 1300
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
410 415 420 425

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ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac 1348
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
430 435 440

agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat 1396
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
445 450 455

gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg 1443
Val Lys Asn Ser Glu Gly Asp Cys Ala
460 465

gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1503

ctgggcacct ggcaccacaa gaccatgttt tctaagaacc atttt 1548

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<211> 466

<212> PRT

<213> Homo sapiens

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20 25 30

Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
35 40 45

Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
50 55 60

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Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
65 70 75 80

Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
85 90 95

Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
100 105 110

Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
115 120 125

Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
130 135 140

Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
145 150 155 160

Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
165 170 175

Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
180 185 190

Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
195 200 205

Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
210 215 220

His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
225 230 235 240

Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
245 250 255

His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
260 265 270

Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
275 280 285

Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
290 295 300

Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
305 310 315 320

Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
325 330 335

Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
340 345 350

Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
355 360 365

Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
370 375 380

Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
385 390 395 400

Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
405 410 415

Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala

420

425

430

Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr

435

440

445

Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp

450

455

460

Cys Ala

465

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gtgaccaagn tcttcccat ggttgaggag atcatgctgc agccacttg ggaatcccga 180

gatcgntacg aggagctgaa gcgntagat gacgccatga aagag

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 gnaaccacca ctgcgccgtg gccttcaga tcctcgccga gcctgagtgn aacatcttct 120
 ccaacatccc acctgatggg ttcaagcaga tccgacag 158

<210> 5
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 <212> DNA
 <213> Homo sapiens

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<220>
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ccaacatccc acctgatggg ttcaagcaga tccgacag

98

<210> 6

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ttcccgtggc cccgttcatg gaccgagaca aagtgaccaa ggccacagcc caggattggg 180
tttcatcaag tttgtcctga tccaatggt tgaacagtg accaagctct tccccatggg 240
ttgagggaga ttcattgctgg cagccanttt ggggaatccc gaggattcgc tacgagggag 300
cttgaagcgg gattaggatg gacggccatg gaaaggagtt ttacaggaag gnaggatttg 360
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<222> 92

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<222> 130

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<221> misc_feature

<222> 390

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<222> 396

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cgccccccgn tttctcagg cacagtctcc ttcactgttt ttcacatctc tgcttctctc 180

tctggacttc tcggtggccc cagacgtcaa gctgtcagtc ttcttctgta actctttcat 240

gggcgtcatc tatccgcttc agctcctcgt aggcgatctc ggggattccc aaagtgggct 300

gcagcatgat cttcctcaac catggggggg aggagcttgg ggcactngtt ttcaaaaatt 360

gggggatcag gggacaaact ttgattggan cccatnttgg ggcttttggg cctttggggc 420

aatttttg 428

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<211> 438

<212> DNA

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<222> 98

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ccagaactgc agccacgccc cccgttttcc tcaggcacag tctccttcac tgtttttcac 180
atctctgntt ctctctctgg gantnttcgg tgggccccag aacgtcaagc tgtcagtntt 240
cttctgtaac tntttcatgg gcgtcatcta tccgtttcag cttcctcgta ggcgatnttg 300
gggattccca aagtgggctg gcagcatgga tcttcctcaa accatggggg gaaggagttt 360
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tgggggntgt gggccttg 438

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tgctgtgata tctccaatga agtccgtccc atggagggtgg cagaatcgtg ggtggactgt 120
ttactggaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180
cattcatgga ccgagacaaa gtgaccaaag caacagccca aattgggttc atcaagtttg 240
tcctgatccc aatgtttgaa ac 262

<210> 10

<211> 250

<212> DNA

<213> Mus musculus

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tgctgtgata tctccaatga agtccgtccc atggagggtgg cagaatcgtg ggtggactgt 120

ttactggaag aatattttat gcagagtgac cgtgagaagt ccgaagcctt cctgtggccc 180

attcatggac cgagacaaag tgaccaaagc aacagccaaa ttgggttcac caagtttgtc 240

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<222> 155

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<221> misc_feature

<222> 393

<223> N = A, T, G, or C

<220>

<221> misc_feature

<222> 442

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cctgggtggg cagccaggcg gttgggctgg cgaanagggt catccatcca gctcacactg 180

gaagccaaga agctgaaatt attagtcttc ttggaacaag gtgtctataa atctggtttt 240
 caagggtcatg actcttacta ggaaagtccg ggcagggcct ccctcctgat gggtcctcct 300
 tcatggtcag aggcagcatt ctcccattcc tccatctctt ttgggatttt gaaggagata 360
 aagtgggggtg aaqcccgtgc attctcgttc tgnntttcca gagaalaaa accagttttc 420
 ccttgaaggc acagccccag cntggcattt tgaaagttg 459

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 Cys His Cys Leu Leu His
 1 5

tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg 164
 Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
 10 15 20

ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc 212
 Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
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25

30

35

atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc 260
 Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe

40

45

50

ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat 308
 Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp

55

60

65

70

cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag 356
 Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln

75

80

85

aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag 404
 Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu

90

95

100

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 453
 Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala

105

110

115

ggggggcgtag gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg 513

aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca 573

ctgatacaaa aaaaaaaaaa aaaaaa 599

<210> 13

<211> 115

<212> PRT

<213> Homo sapiens

<400> 13

Cys His Cys Leu Leu His Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu
 1 5 10 15

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 20 25 30

Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu
 35 40 45

Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro
 50 55 60

Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp
 65 70 75 80

Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala
 85 90 95

Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly
 100 105 110

Asp Cys Ala
 115

<210> 14

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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agtcgaattc accgtgagaa gtcagaag

28

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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gtcaaagctt acatggtctt gtggtgcc

28

<210> 16

<211> 1303

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107)..(1066)

<400> 16

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cttactaacg ttagcccccga gcctagctat ggaggggtgca tgctga gcc ctg gag 115

Ala Leu Glu

1

cac atg tac cac gac ctc ggg ctg gtc agg gac ttc agc atc aac cct 163

His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro

5

10

15

gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac aac tac aga aac 211
 Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn
 20 25 30 35

aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg 259
 Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met
 40 45 50

tac agc atg gtc tgg ctc tgc agt ctc cag gag aag ttc tca caa acg 307
 Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr
 55 60 65

gat atc ctg atc cta atg aca gcg gcc atc tgc cac gat ctg gac cat 355
 Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His
 70 75 80

ccc ggc tac aac aac acg tac cag atc aat gcc cgc aca gag ctg gcg 403
 Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala
 85 90 95

gtc cgc tac aat gac atc tca ccg ctg gag aac cac cac tgc gcc gtg 451
 Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val
 100 105 110 115

gcc ttc cag atc ctc gcc gag cct gag tgc aac atc ttc tcc aac atc 499
 Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile
 120 125 130

cca cct gat ggg ttc aag cag atc cga cag gga atg atc aca tta atc 547
 Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile
 135 140 145

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ttg gcc act gac atg gca aga cat gca gaa att atg gat tct ttc aaa 595
 Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys
 150 155 160

gag aaa atg gag aat ttt gac tac agc aac gag gag cac atg acc ctg 643
 Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu
 165 170 175

ctg aag atg att ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt 691
 Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg
 180 185 190 195

cca atg gaa gtc gca gag cct tgg gtg gac tgt tta tta gag gaa tat 739
 Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr
 200 205 210

ttt atg cag agc gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg 787
 Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro
 215 220 225

ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc 835
 Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe
 230 235 240

atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc 883
 Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe
 245 250 255

ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat 931
 Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp
 260 265 270 275

cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag 979
 Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln
 Page 21

280

285

290

aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag 1027

Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu

295

300

305

aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc 1076

Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala

310

315

320

ggggggcggtg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg 1136

aagagctgcc ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca 1196

ctgatacaaa aaaaaaaaaag gaattcatga tgctgtacag aattttatatt ttaaactgtc 1256

ttttaaataa tatattctta tacggaaaaa aaaaaaaaaa aaaaaaa 1303

<210> 17

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<213> Homo sapiens

<400> 17

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Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp Asn

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25

30

Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val Ala

35

40

45

37993.txt

Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys Phe
 50 55 60

Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His Asp
 65 70 75 80

Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg Thr
 85 90 95

Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His His
 100 105 110

Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile Phe
 115 120 125

Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile
 130 135 140

Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp
 145 150 155 160

Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His
 165 170 175

Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn
 180 185 190

Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu
 195 200 205

Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro
 210 215 220

Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln
 Page 23

225	230	235	240
Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr			
245	250	255	
Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu			
260	265	270	
Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys			
275	280	285	
Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys			
290	295	300	
Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala			
305	310	315	320

<210> 18

<211> 1887

<212> DNA

<213> Homo sapiens

<220>

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<222> (74)..(1672)

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 Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala

1

5

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37993.txt

145	150	155	
agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag			589
Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys			
160	165	170	
aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc			637
Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu			
175	180	185	
tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg			685
Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp			
190	195	200	
ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac			733
Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His			
205	210	215	220
gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg			781
Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg			
225	230	235	
agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac			829
Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His			
240	245	250	
aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc			877
Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val			
255	260	265	
tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc			925
Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile			
270	275	280	

37993.txt

cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac	973
Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn	
285 290 295 300	
aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat	1021
Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn	
305 310 315	
gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc	1069
Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile	
320 325 330	
ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg	1117
Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly	
335 340 345	
ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac	1165
Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp	
350 355 360	
atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag	1213
Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu	
365 370 375 380	
aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att	1261
Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile	
385 390 395	
ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc	1309
Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val	
400 405 410	
gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc	1357
Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser	

415	420	425	
gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga			1405
Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg			
430	435	440	
gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc			1453
Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val			
445	450	455	460
ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag			1501
Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu			
	465	470	475
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag			1549
Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu			
	480	485	490
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac			1597
Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp			
	495	500	505
agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat			1645
Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp			
	510	515	520
gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg			1692
Val Lys Asn Ser Glu Gly Asp Cys Ala			
525	530		
gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc			1752
ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca ctgataaaaa			1812

aaaaaaaaa ggaattcatg atgctgtaca gaattttatt tttaaactgt cttttaata 1872

atatattctt atacg 1887

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<212> PRT

<213> Homo sapiens

<400> 19

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1 5 10 15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser

20 25 30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn

35 40 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp

50 55 60

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro

65 70 75 80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val

85 90 95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu

100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val

115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
 130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
 145 150 155 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
 165 170 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
 180 185 190

Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
 195 200 205

Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
 210 215 220

Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
 225 230 235 240

Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
 245 250 255

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser
 260 265 270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala
 275 280 285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln
 290 295 300

37993.txt

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro
305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro
325 330 335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile
340 345 350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His
355 360 365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr
370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys
385 390 395 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
420 425 430

Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr
435 440 445

Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met
450 455 460

Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu
465 470 475 480

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile
Page 31

485

490

495

Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser

500

505

510

Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser

515

520

525

Glu Gly Asp Cys Ala

530

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<211> 1967

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(1741)

<400> 20

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10

15

tgc aac tcc agc gac atc atg gac ctg ttc tgc atc gcc acc ggc ctg 97

Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu

20

25

30

cct cgg aac acg acc atc tcc ctg ctg acc acc gac gac gcc atg gtc 145

Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val

35

40

45

180	185	190	
aag aag atg agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc			625
Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys			
195	200	205	
ccc tgt aag tac agt ttt ttg gat aac cac aag aag ttg act cct cga			673
Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg			
210	215	220	
cgc gat gtt ccc act tac ccc aag tac ctg ctc tct cca gag acc atc			721
Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile			
225	230	235	240
gag gcc ctg cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat			769
Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn			
245	250	255	
gag atg ctg agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc			817
Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val			
260	265	270	
agg gac ttc agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc			865
Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys			
275	280	285	
gtc cac gac aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc			913
Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys			
290	295	300	
ttc tgc gtg gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc			961
Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu			
305	310	315	320

37993.txt

cag gag aag ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc 1009
 Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
 325 330 335

atc tgc cac gat ctg gac cat ccc ggc tac aac aac acg tac cag atc 1057
 Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile
 340 345 350

aat gcc cgc aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg 1105
 Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
 355 360 365

gag aac cac cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag 1153
 Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
 370 375 380

tgc aac atc ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga 1201
 Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
 385 390 395 400

cag gga atg atc aca tta atc ttg gcc act gac atg gca aga cat gca 1249
 Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
 405 410 415

gaa att atg gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc 1297
 Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
 420 425 430

aac gag gag cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt 1345
 Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
 435 440 445

gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg 1393
 Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
 Page 35

450	455	460	
gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca			1441
Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser			
465	470	475	480
gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag			1489
Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys			
485	490	495	
gcc aca gcc cag att ggg ttc atc aag ttt gtc ctg atc cca atg ttt			1537
Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe			
500	505	510	
gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag			1585
Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln			
515	520	525	
cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cgg ata gat			1633
Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp			
530	535	540	
gac gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg			1681
Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly			
545	550	555	560
gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa			1729
Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu			
565	570	575	
gga gac tgt gcc tgaggaaagc ggggggctgt gctgcagttc tggacgggct			1781
Gly Asp Cys Ala			
580			

37993.txt

ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc ctgggcacct ggcaccacaa 1841

gaccatgttt tctaagaacc attttgttca ctgatacaaa aaaaaaaaaa ggaattcatg 1901

atgctgtaca gaattttatt tttaaactgt cttttaaata atatattctt atacggaaaa 1961

aaaaaa 1967

<210> 21

<211> 580

<212> PRT

<213> Homo sapiens

<400> 21

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Cys Asn Ser Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu

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Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val

35 40 45

Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys

50 55 60

Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys

65 70 75 80

Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg

85 90 95

Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser

100

105

110

Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu

115

120

125

Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu

130

135

140

Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu

145

150

155

160

Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu

165

170

175

Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile

180

185

190

Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys

195

200

205

Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg

210

215

220

Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile

225

230

235

240

Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn

245

250

255

Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val

260

265

270

Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys

275

280

285

Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys
290 295 300

Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu
305 310 315 320

Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala
325 330 335

Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile
340 345 350

Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu
355 360 365

Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu
370 375 380

Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg
385 390 395 400

Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala
405 410 415

Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser
420 425 430

Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys
435 440 445

Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val
450 455 460

37993.txt

Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser
465 470 475 480

Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
485 490 495

Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe
500 505 510

Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln
515 520 525

Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
530 535 540

Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly
545 550 555 560

Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu
565 570 575

Gly Asp Cys Ala
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<211> 1457

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (164)..(1453)

<400> 22

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ggaaagtaca gtaaaaagtc cgagtgcagc cgccggggcg agg atg gga tcc ggc 175

Met Gly Ser Gly

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tcc tcc agc tac cgg ccc aag gcc atc tac ctg gac atc gat gga cgc 223

Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg

5

10

15

20

att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271

Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met

25

30

35

gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc 319

Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser

40

45

50

ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc 367

Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro

55

60

65

gcg aat tca gaa cgc act ccg tac aaa gtg aga cct gtg gcc atc aag 415

Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys

70

75

80

caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt 463

Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val

85

90

95

100

gca gag cag ttc tca aga gca ttc aaa atc aat gaa ctg aaa gct gaa 511

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37993.txt

Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu	
105	110 115
gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa ttg gaa gga	559
Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly	
120	125 130
cta aaa gtg gtg gaq att gag aaa tgc aag agt gac att aag aag atg	607
Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met	
135	140 145
agg gag gag ctg gcg gcc aga agc agc agg acc aac tgc ccc tgt aag	655
Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys	
150	155 160
tac agt ttt ttg gat aac cac aag aag ttg act cct cga cgc gat gtt	703
Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val	
165	170 175 180
ccc act tac ccc aag tac ctg ctc tct cca gag acc atc gag gcc ctg	751
Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu	
185	190 195
cgg aag ccg acc ttt gac gtc tgg ctt tgg gag ccc aat gag atg ctg	799
Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu	
200	205 210
agc tgc ctg gag cac atg tac cac gac ctc ggg ctg gtc agg gac ttc	847
Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe	
215	220 225
agc atc aac cct gtc acc ctc agg agg tgg ctg ttc tgc gtc cac gac	895
Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp	
230	235 240


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aac tac aga aac aac ccc ttc cac aac ttc cgg cac tgc ttc tgc gtg 943
Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val
245                250                255                260

gcc cag atg atg tac agc atg gtc tgg ctc tgc agt ctc cag gag aag 991
Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys
                265                270                275

ttc tca caa acg gat atc ctg atc cta atg aca gcg gcc atc tgc cac 1039
Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His
                280                285                290

gat ctg gac cat ccc ggc tac aac aac acg tac cag atc aat gcc cgc 1087
Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg
                295                300                305

aca gag ctg gcg gtc cgc tac aat gac atc tca ccg ctg gag aac cac 1135
Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His
                310                315                320

cac tgc gcc gtg gcc ttc cag atc ctc gcc gag cct gag tgc aac atc 1183
His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile
                325                330                335                340

ttc tcc aac atc cca cct gat ggg ttc aag cag atc cga cag gga atg 1231
Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met
                345                350                355

atc aca tta atc ttg gcc act gac atg gca aga cat gca gaa att atg 1279
Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met
                360                365                370

gat tct ttc aaa gag aaa atg gag aat ttt gac tac agc aac gag gag 1327
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Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu
 375 380 385

cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt gat atc tct 1375
 His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser
 390 395 400

aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg gac tgt tta 1423
 Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu
 405 410 415 420

tta gag gaa tat ttt atg cag agc gac cgt gaga 1457
 Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg
 425 430

<210> 23

<211> 430

<212> PRT

<213> Homo sapiens

<400> 23

Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
 1 5 10 15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
 20 25 30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
 35 40 45

Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
 50 55 60

37993.txt

Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
65 70 75 80

Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
85 90 95

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu
100 105 110

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val
115 120 125

Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp
130 135 140

Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn
145 150 155 160

Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro
165 170 175

Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr
180 185 190

Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro
195 200 205

Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu
210 215 220

Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe
225 230 235 240

Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His
Page 45

245

250

255

Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser

260

265

270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala

275

280

285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln

290

295

300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro

305

310

315

320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro

325

330

335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile

340

345

350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His

355

360

365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr

370

375

380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys

385

390

395

400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp

405

410

415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg

420

425

430

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG epitope

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Asp Thr Lys Asp Asp Asp Asp Lys

1

5

<210> 25

<211> 54

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

37993.txt

<400> 26

cgaggagtca acttcttg

18